

SEQ.Listing.ST25  
SEQUENCE LISTING



<110> Cooke, Michael P.  
Sauer, Karsten  
Wiltshire, Tim  
Tarantino, Lisa  
Fletcher, Colin  
Wen, Ben

<120> METHODS AND COMPOSITIONS FOR MODULATING T LYMPHOCYTES

<130> P1097US10

<140> US 10/764,330  
<141> 2004-01-23

<150> US 60/442,792  
<151> 2003-01-25

<160> 4

<170> PatentIn version 3.2

<210> 1  
<211> 1192  
<212> PRT  
<213> Mus musculus

<400> 1

Thr Pro Pro Pro Cys Leu Arg Glu Phe Leu Phe Ser Leu Cys Leu His  
1 5 10 15

Ser Arg Glu Ile Val Tyr Gly Ala Trp Gly Gly Gly Arg Ala Arg Asp  
20 25 30

Phe Ala Leu Cys Pro Pro Pro Arg Pro Cys Cys Ser Ile Ser Ala Gln  
35 40 45

Ser Tyr Gly Arg Arg Ala Ser Gly Thr Lys Pro Arg Ala Ala Gly Gly  
50 55 60

Gly Gly Ala Gly Gly Gly Ala Gly Arg Arg Ala Ala Ala Ala Gly Gly  
65 70 75 80

Pro Cys Thr Met Ala Val Tyr Cys Tyr Ala Leu Asn Ser Leu Val Ile  
85 90 95

Met Asn Ser Thr Asn Glu Leu Lys Ser Gly Gly Pro Arg Pro Ser Gly  
100 105 110

Ser Glu Thr Pro Gln Pro Ser Gly Arg Ala Ala Leu Ser Pro Gly Ser  
115 120 125

Val Phe Ser Pro Gly Arg Gly Ala Ser Phe Leu Phe Pro Pro Ala Glu  
Page 1

SEQ.Listing.ST25  
140

130

135

Ser Leu Ser Leu Glu Glu Pro Gly Ser Pro Gly Gly Trp Arg Ser Gly  
145 150 155 160

Arg Arg Arg Leu Asn Ser Ser Ser Gly Ser Gly Gly Gly Ser Ser Ser  
165 170 175

Ser Asn Ser Ser Ser Ser Ser Gly Val Gly Ser Pro Ser Trp Ala Gly  
180 185 190

Arg Leu Arg Gly Asp Ala Gln Gln Val Val Ala Ala Arg Ile Leu Ser  
195 200 205

Pro Pro Gly Pro Glu Glu Ala Gln Arg Lys Leu Arg Ile Leu Gln Arg  
210 215 220

Glu Leu Gln Asn Val Gln Val Asn Gln Lys Val Gly Met Phe Glu Ala  
225 230 235 240

Gln Ile Gln Ala Gln Ser Ser Ala Ile Gln Ala Pro Arg Ser Pro Arg  
245 250 255

Leu Gly Arg Ala Arg Ser Pro Ser Pro Cys Pro Phe Arg Ser Ser Ser  
260 265 270

Gln Pro Pro Glu Arg Val Leu Ala Pro Cys Ser Pro Ser Glu Glu Arg  
275 280 285

Arg Thr Lys Ser Trp Gly Glu Gln Cys Thr Glu Thr Pro Asp Thr Asn  
290 295 300

Ser Gly Arg Arg Ser Arg Leu Ser Thr His Pro Ser Lys Asp Lys Glu  
305 310 315 320

Gly Val Ala Pro Leu Leu Gly Pro Ala Ser Pro Thr Arg Leu Gly Thr  
325 330 335

Gln Ser Pro Ser Thr Ser Val Arg Met Glu Arg Gly Thr Pro Ala Ser  
340 345 350

Pro Arg Cys Gly Ser Pro Thr Pro Met Glu Thr Asp Lys Arg Val Ala  
355 360 365

Pro Ser Leu Glu Arg Phe Gly Thr Ser Leu Thr Leu Ala Thr Lys Val  
370 375 380

SEQ.Listing.ST25

Ala Ala Ser Ala Ala Ser Ala Gly Pro His Pro Gly His Asp Ser Ala  
385 390 395 400

Leu Met Glu Thr Gly Cys Glu Leu Gly Gly Met Arg Pro Trp Glu Ala  
405 410 415

Gln Met Glu Arg Arg Gly Gln Phe Leu Gly Lys Glu Thr Gly Ser Thr  
420 425 430

Pro Glu Pro Val Arg Thr His Met Arg Glu Pro Pro Gly Arg Val Gly  
435 440 445

Arg Gly Ile His Ser Val Gly Gly Gln Gly Ser Trp Thr Pro Glu Val  
450 455 460

Ile Lys Arg Pro Glu Glu Arg Ala Val Thr Ala Gln Ser Ser Glu Pro  
465 470 475 480

Ser Glu Asp Pro Arg Trp Ser Arg Leu Pro Val Asp Leu Asp Ser Val  
485 490 495

Gly Pro Glu Lys Gly Gly Asn Arg Ile Pro Gly Met Arg Gly Pro Gln  
500 505 510

Gln Thr Leu Asp Ser Glu Arg Glu Gly Ser Pro Ala Leu Gly Leu Leu  
515 520 525

Gly Gly Ser Gln Ala Ala Gln Pro Gly Ala Arg Gly Val Glu Glu Asp  
530 535 540

Val His Tyr Gly Arg Met Leu Glu Pro Leu Pro Pro Gly Glu Val Thr  
545 550 555 560

Thr Lys Leu Lys Glu Pro Gln Cys Leu Pro Gly Asp Arg Met Gly Met  
565 570 575

Gln Pro Glu Ser Ser Ile Val Trp Pro Ser Ala Leu Glu Glu Ala Pro  
580 585 590

Leu Ile Trp Thr Arg Asp Thr Gly Val Gln Ser Lys Gly Thr Trp Gly  
595 600 605

Ser Gln Leu Pro Asp Gly Asp Ala His Pro Ser Cys Gln Glu Met Pro  
610 615 620

Pro Asp Gln Lys Asp Lys Ala Ser Leu Lys Glu Ala Cys Ser Pro Ser  
625 630 635 640

SEQ.Listing.ST25

Asn Ile Pro Ala Ile Pro Ala Val Ile Ile Thr Asp Met Gly Ala Gln  
 645 650 655  
 Glu Asp Gly Gly Leu Glu Glu Ile Gln Gly Ser Pro Arg Gly Pro Leu  
 660 665 670  
 Pro Leu Arg Lys Leu Ser Ser Ser Ala Ser Ser Thr Gly Phe Ser  
 675 680 685  
 Ser Ser Tyr Asp Asp Ser Glu Glu Asp Ile Ser Ser Asp Pro Glu Arg  
 690 695 700  
 Thr Leu Asp Pro Asn Ser Ala Phe Leu His Thr Leu Asp Gln Gln Lys  
 705 710 715 720  
 Pro Arg Val Ser Lys Ser Trp Arg Lys Ile Lys Asn Met Val Gln Trp  
 725 730 735  
 Ser Pro Phe Val Met Ser Phe Lys Lys Lys Tyr Pro Trp Ile Gln Leu  
 740 745 750  
 Ala Gly His Ala Gly Ser Phe Lys Ala Ala Ala Asn Gly Arg Ile Leu  
 755 760 765  
 Lys Lys His Cys Glu Ser Glu Gln Arg Cys Leu Asp Arg Leu Met Ala  
 770 775 780  
 Asp Val Leu Arg Pro Phe Val Pro Ala Tyr His Gly Asp Val Val Lys  
 785 790 795 800  
 Asp Gly Glu Arg Tyr Asn Gln Met Asp Asp Leu Leu Ala Asp Phe Asp  
 805 810 815  
 Ser Pro Cys Val Met Asp Cys Lys Met Gly Val Arg Thr Tyr Leu Glu  
 820 825 830  
 Glu Glu Leu Thr Lys Ala Arg Lys Lys Pro Ser Leu Arg Lys Asp Met  
 835 840 845  
 Tyr Gln Lys Met Val Glu Val Asp Pro Glu Ala Pro Thr Glu Glu Glu  
 850 855 860  
 Lys Ala Gln Arg Ala Val Thr Lys Pro Arg Tyr Met Gln Trp Arg Glu  
 865 870 875 880  
 Thr Ile Ser Ser Thr Ala Thr Leu Gly Phe Arg Ile Glu Gly Ile Lys  
 885 890 895

SEQ.Listing.ST25

Lys Glu Asp Gly Ser Val Asn Arg Asp Phe Lys Lys Thr Lys Thr Arg  
 900 905 910  
 Glu Gln Val Thr Glu Ala Phe Arg Glu Phe Thr Lys Gly Asn Gln Asn  
 915 920 925  
 Ile Leu Ile Ala Tyr Arg Asp Arg Leu Lys Ala Ile Arg Ala Thr Leu  
 930 935 940  
 Glu Ile Ser Pro Phe Phe Lys Cys His Glu Val Ile Gly Ser Ser Leu  
 945 950 955 960  
 Leu Phe Ile His Asp Lys Lys Glu Gln Ala Lys Val Trp Met Ile Asp  
 965 970 975  
 Phe Gly Lys Thr Thr Pro Leu Pro Glu Gly Gln Thr Leu Gln His Asp  
 980 985 990  
 Val Pro Trp Gln Glu Gly Asn Arg Glu Asp Gly Tyr Leu Ser Gly Leu  
 995 1000 1005  
 Asp Asn Leu Ile Asp Ile Leu Thr Glu Met Ser Gln Gly Ser Pro  
 1010 1015 1020  
 Leu Thr Gly His Arg His Arg Ala Pro Cys His Phe Ala Arg His  
 1025 1030 1035  
 Leu Cys Leu Ser Pro Leu Ser Ser Pro Asn Ser Ser Phe Ser Cys  
 1040 1045 1050  
 Leu Ser Ala Tyr Leu Glu Gln Ser Leu Pro Ser Ala Leu Gln Asp  
 1055 1060 1065  
 Thr Leu Glu Lys Lys Lys Arg Phe Phe Phe Ser Arg Ser Leu Leu  
 1070 1075 1080  
 Pro Arg Pro Pro Thr Gly Leu Gly Gly Gly Val Ser His Ala Leu  
 1085 1090 1095  
 Ile Glu Pro Pro Ser Arg Arg Glu Leu His Lys Ala Arg Pro His  
 1100 1105 1110  
 Ile Leu Leu His Ser Glu Ser Ala Arg Val Gln Lys Ala Val Ser  
 1115 1120 1125  
 Leu Val Ala Ser Leu Glu Arg Leu Ser Leu Pro Leu Gly Asp Thr

SEQ.Listing.ST25  
1140

1130

1135

Ala Pro Leu Pro Glu Asn Ser Gly Pro His Trp Leu Pro Val Gly  
1145 1150 1155

Ala Leu Leu Pro Pro Ser Gly Cys His Gln Ala Gln Ser His Leu  
1160 1165 1170

Cys Leu Ser Pro Arg Ala Leu Lys Pro Gly Gln Gly Pro Asp Phe  
1175 1180 1185

Trp Glu Leu Glu  
1190

<210> 2  
<211> 2841  
<212> DNA  
<213> Homo sapiens

<400> 2  
atggctgtgt actgctatgc gctcaatagc ctggtgatca tgaatagcgc caacgagatg 60  
aagagcggcg gcggcccggg gccagtgagg agcgagacgc ccccgcccc gaggagggca 120  
gtgctgagcc ccggcagcgt ttccagcccc gggagaggcg cctctttcct cttcccccca 180  
gccgagtcgc tgtccccga ggagccccgg agccccgggg gctggcggag cggccggcgc 240  
aggctgaata gtagcagcgg cagtggcagc ggcagcagcg gcagtagcgt gagcagccca 300  
agttgggctg gtcgcctgcg aggggaccgg cagcaggtgg tggcagccgg taccctctcc 360  
ccgccagggc cggaggaggc caagaggaag ctgaggatct tgcagcgcga gttgcagaac 420  
gtgcaggtga accagaaagt gggcatgttt gaggcgcaca tccaggcaca gagctccgcc 480  
attcaagcgc cccgcagccc gcgtttgggc agggctcgct cgccctcccc gtgccccttc 540  
cgcagcagca gtcagcccc tggaaagggc ctggttcagg gcgcccggag cgaggaacgg 600  
aggacaaagt cctgggggga gcaatgtcca gagacttcag gaaccgactc cgggaggaaa 660  
ggagggccca gcctatgctc ctgcaggtg aagaaaggaa tgccacctct tcccggccgg 720  
gctgccccta caggatcaga ggctcagggt ccatccgctt ttgtaaggat ggagaagggt 780  
atccctgcc agtccccgctg tggctcacc acagctatgg aaattgacaa aaggggctct 840  
cctaccccgg gaactcggag ctgcctagct ccctcattgg ggctgttcgg agctagctta 900  
acgatggcca cggaagtggc agcgagagtt acatccactg ggccacaccg tccacaggat 960  
cttgccctca ctgagccgctc tgggagagcc cgtgagcttg aggacctgca gccccagag 1020  
gccctggtgg agaggcaggg gcagtttctg ggcagtgaga caagcccagc cccagaaagg 1080  
ggcgggcccc gcgatggaga accccctggg aagatgggga aaggatatct gccctgtggc 1140

SEQ.Listing.ST25

atgccgggct	ctgggggagcc	tgaagtgggc	aaaaggccag	aggagacgac	tgtgagcgtg	1200
caaagcgcag	agtcctctga	tgccctgagc	tggtccaggc	tgcccagggc	cctggcctcc	1260
gtaggccctg	aggaggcccg	aagtggggcc	cccgtgggcg	gggggcgttg	gcagctctcc	1320
gacagagtgg	agggagggtc	cccaacgctg	ggcttgcttg	ggggcagccc	ctcagcacag	1380
ccggggaccg	ggaatgtgga	ggcgggaatt	ccttctggca	gaatgctgga	gcctttgccc	1440
tgttgggacg	ctgcgaaaga	tctgaaagaa	cctcagtgcc	ctcctgggga	caggggtgggt	1500
gtgcagcctg	ggaactccag	ggtttggcag	ggcaccatgg	agaaagccgg	tttggcttgg	1560
acgcgtggca	caggggtgca	atcagagggg	acttgggaaa	gccagcggca	ggacagtgat	1620
gccctcccaa	gtccggagct	gctaccccaa	gatcaggaca	agcctttcct	gaggaaggcc	1680
tgacgcccc	gcaacatacc	tgctgtcatc	attacagaca	tgggcaccca	ggaggatggg	1740
gccttgagg	agacgcagg	aagccctcgg	ggcaacctgc	ccctgaggaa	actgtcctct	1800
tcctcggcct	cctccacggg	cttctcctca	tcctacgaag	actcagagga	ggacatctcc	1860
agtgaccctg	agcgcaccct	ggaccccaac	tcagctttcc	tgcataccct	ggaccagcag	1920
aaacctagag	tgagcaaatc	atggaggaag	ataaaaaaca	tggtgcactg	gtctcccttc	1980
gtcatgtcct	tcaagaagaa	gtacccttgg	atccagctgg	caggacacgc	agggagtttc	2040
aaggcagctg	ccaatggcag	gatcctgaag	aagcactgtg	agtcagagca	gcgctgcctg	2100
gaccggctga	tggtggatgt	gctgaggccc	ttcgtacctg	cctaccatgg	ggatgtggtg	2160
aaggacgggg	agcgtacaa	ccagatggac	gacctgctgg	ccgacttcga	ctcgccctgt	2220
gtgatggact	gcaagatggg	aatcaggacc	tacctggagg	aggagctcac	gaaggcccgg	2280
aagaagccca	gcctgcggaa	ggacatgtac	cagaagatga	tcgaggtgga	ccccgaggcc	2340
cccaccgagg	aggaaaaagc	acagcgggct	gtgaccaagc	cacggtacat	gcagtggcgg	2400
gagaccatca	gctccacggc	caccctgggg	ttcaggatcg	agggaatcaa	aaaagaagac	2460
ggcaccgtga	accgggactt	caagaagacc	aaaacgaggg	agcaggtcac	cgaggccttc	2520
agagagttca	ctaaaggaaa	ccataacatc	ctgatcgcct	atcgggaccg	gctgaaggcc	2580
attcgaacca	ctctagaagt	ttctcccttc	ttcaagtgcc	acgaggtcac	tggcagctcc	2640
ctcctcttca	tccacgacaa	gaaggaacag	gccaaagtgt	ggatgatcga	ctttgggaaa	2700
accacgcccc	tgcttgaggg	ccagaccctg	cagcatgacg	ttccctggca	ggaggggaac	2760
cgggaggatg	gctacctctc	ggggctcaat	aacctcgtcg	acatcctgac	cgagatgtcc	2820
caggatgccc	cactcgcttg	a				2841

<210> 3  
 <211> 2805  
 <212> DNA  
 <213> Rattus norvegicus

# SEQ.Listing.ST25

```

<400> 3
atggctgtgt actgctatgc cctcaatagc ctggtgatca tgaacagcac caacgagctg 60
aagagtggca gccccctgcc cagcggcagc gaaacgcctc agccctccgg gagggccgcg 120
ctgagccccg gcagcgtctt cagccctggg agaggcgcct cttttctctt cccccagca 180
gagtcgctgt cgctggagga gcctgggagt gctgggggtt ggcgcagcgg ccgacggagg 240
ctgaatagta gcagcggtag cggaggtggc agcagcagca gcaacagcag cagcagcagt 300
ggcgtgggca gtcccagttg ggctggccgc ctgcgagggg acgcgcagca ggtggtggcg 360
acccgcatcc tctccccacc tgggccggag gagggcccaga ggaagctgag gattctgcag 420
cgcgaattgc aaaatgtgca ggtgaaccag aaagtgggca tgttcgaggc gcaaattccag 480
gcacagacct ctgctattca agcgcctcga agcccgcggt tgggtagggc tcgttcgccc 540
tccccgtgtc ctttcgaag cagcagccag cctcctgaaa gggctcttggc tccatgttcc 600
ccaagtgagg aacggagaac aaagtcctgg ggagaacaat gtacagagac cccagatgcc 660
aactccagga ggagaagcag actcagcaca caccctcga aggacaagga gggagtggcc 720
cctcttttag gccagccag cccgaccagg ttagggactc agagtccatc tacttcagtg 780
agaatggaaa gaggttcccc ggccagtccc cgctgtggct caccacacc catggaaatt 840
gacaagagga ctgctccctc actggagcac tttgggacta gcttaacgtt ggccactaaa 900
gtggcagctt cggccgcata cgctggacca caccctggac atgattctgt tctcatggag 960
gcagactgtg agctaggggg catgcgcccc tgggaggccc acctggagag acggggggcag 1020
tttctgggca gggagaccgg ctacgcccca gagcctatcc ggaccacat tagagaaccc 1080
cctggaaggg tggaaagagt tcattctgtt ggtggccagg gtcctggac acctgaagtc 1140
atcaaaagac cagaagaggg aactgtggat gcccaaagct cagagctctc agagaacccg 1200
agatggtcta gactgcctgg agaccgggt tccgtagggc ctgagaaggg aggtagtagg 1260
atcccaggaa tccgaggacc ccagcagacc ctggacagca tgagagaagg gtcttcagca 1320
ctgggcttgc ttggggggcag ccaggcagca cagccaggga gcatggatgt ggagacaggc 1380
attagttgtg gcagaatgct ggaaccctta ccacctgggg aagtaacaac aaatttgaaa 1440
gaaccccagt gcctccctgg ggacaggatg gggatgcagc ctgagagttc catagtttgg 1500
cccagtgtg tggaggaagc tcccctgatc tggacgtgtg acacagggat acagttaaag 1560
gggacttggg gaagccaaga tggagatgct catcctagct gccaagagaa gtccccagac 1620
cagaaggaca aggcctgcag ccccagcaac atcccgcca tccctgcagt catcattaca 1680
gatatgggtg ctcaggagga tggagggtta gaggagatcc aaggaagccc tcgggggtccc 1740
ctgcctctga ggaagctgtc gtcctcctca gcctcctcca ctggcttctc ctcttcctat 1800
gaggactcgg aggaggacat ctccagtgc cctgagcgca ctctggaccc caactcagcc 1860

```



SEQ.Listing.ST25

tttttgcata	ccttggacca	gcagaagccc	agagtgagca	agtcatggag	gaagataaag	1920
aacatggtgc	agtgggtcccc	ctttgtcatg	tccttcaaga	agaagtaccc	ctggatccag	1980
ctggcaggac	atgcagggag	cttcaaggca	gctgcgaatg	gccgtatcct	taagaagcat	2040
tgtgagtctg	aacagcgatg	cctggaccgg	ttaatggcgg	atgtgctgag	gcccttcgtg	2100
ccagcctacc	atggcgacgt	ggtgaaggac	ggggaacgct	acaaccagat	ggacgacctg	2160
ctggctgact	tcgattcacc	ctgcgtgatg	gactgcaaga	tgggcatcag	gacataacctg	2220
gaggaagaac	tcaccaaggc	ccggaagaag	cctagcttgc	ggaaggacat	gtaccagaag	2280
atggtggagg	tggaccctga	ggccccact	gaagaggaga	aagcccagag	agctgtgacc	2340
aagccacgtt	atatgcagtg	gcgggaaacc	atcagttcca	cagctacctt	aggcttcagg	2400
atcgagggca	tcaagaagga	agatggctct	gtgaaccgtg	acttcaagaa	gaccaaaca	2460
agggagcagg	tcactgaggc	cttcagagaa	ttcactaaag	gaaaccagaa	catcctgatt	2520
gcctaccggg	accggttgaa	ggccattcga	gaaaccctgg	aagtctctcc	cttcttcaag	2580
tgccatgagg	tcattggcag	ctctctcctc	ttcatccacg	acaagaagga	gcaagccaag	2640
gtgtggatga	ttgactttgg	gaaaaccacg	ccccttcgg	aaggccagac	cctacaacac	2700
gatgtcccct	ggcaggaggg	gaaccgggag	gatggctacc	tctcagggct	gaacaacctc	2760
atcgacatcc	tgacagaaat	gtcccagggc	agcccactca	cctga		2805

<210> 4  
 <211> 3608  
 <212> DNA  
 <213> Mus musculus

<400> 4	
caccccaccc	ccttgatgcc ttcgggaatt ctgacttttc tccttgtgtc tccacagccg 60
cgaaatcggt	tatggagctt ggggcggggg ccgagcccgc gattttgccc tgtgcccgcc 120
gcctaggcca	tgctgctcca tcagcgcgca gagctacggc cgccgggcct ccgggactaa 180
gccgagagcc	gcgggaggag gaggcgccgg cgggtggagcg ggacggagag ccgcggcggc 240
gggcggaccc	tgtactatgg ctgtgtactg ctatgccctc aatagcctgg tgatcatgaa 300
cagcaccaac	gagctcaaga gtggcggccc ccggcccagc ggcagcgaga cgccccagcc 360
ctccgggagg	gccgcgctga gtcccggcag cgtcttcagc cctgggagag gcgcttcctt 420
tctcttcccc	ccagcagagt cgctgtccct ggaggagccc gggagtcctg ggggctggcg 480
cagcggccgg	cgcaggctga atagtagcag cggtagcggg ggtggcagca gcagcagcaa 540
cagcagcagc	agcagtggcg tgggcagtcc cagttgggct ggccgcctgc gaggggacgc 600
gcagcaggtg	gtggcggccc gcatcctctc cccacctggg ccagaggagg cccagaggaa 660
gctgcggatt	ctgcagcgcg agttgcaaaa tgtgcaggtg aaccagaaag tgggcatggt 720

SEQ.Listing.ST25

cgaggcgcaa atccaggcac agagctctgc cattcaagcg ccccgaagcc cgcgtttggg	780
tagggctcgt tcgccctccc cgtgtccctt ccgaagtagc agccagcccc ccgaaaggg	840
cttggctccg tgttctccaa gtgaggaacg cagaacaaag tcctggggag aacaatgtac	900
agaaaccca gataccaact ctggaaggag aagcagactc agcacacacc cctcgaagga	960
caaggaggga gtggcccctc ttttagggcc agccagcccc accaggttag ggactcagag	1020
tccatctact tccgtgagaa tggaaagagg taccctggcc agtccccgct gtggctcacc	1080
cacacccatg gaaactgaca agaggggtgc tccctcactg gagcgctttg gaactagctt	1140
aacgttggct actaaagtgg cagcttcagc cgcattccgct ggaccacacc ctggacatga	1200
ttctgccctc atggagacag gctgtgagct cgggggcatg cggccctggg agggccagat	1260
ggagagacgg gggcagtttc tgggcaagga gaccggctca accccagagc ctgtccggac	1320
ccacatgaga gaaccccctg gaaggggtgg aagaggaatt cattctgttg gtgggcaggg	1380
ctcctggaca cctgaagtca tcaaaagacc agaagagagg gctgtgactg cccaaagctc	1440
agagccctca gaggacccca gatgggtctag actgcctgta gacctggatt ccgtaggacc	1500
tgagaaggga ggaaatagga tcccagggat gcgaggggcc cagcagaccc tggacagtga	1560
gagagaaggc tctccagcac tgggcttgct tgggggcagc caggcagcac agccaggggc	1620
taggggtgtg gaggaagacg ttcattatgg ccgaatgctg gaacctttac cacctgggga	1680
agtaacaaca aaattgaaag aaccccagtg cctccctggg gacaggatgg gaatgcagcc	1740
tgagagttcc atagtttggc ccagtgccct ggaggaagct cccctgatct ggacacgtga	1800
cacgggggta cagtcgaagg ggacttgggg aagccagctg ccagacggag atgctcacc	1860
tagctgccaa gagatgcccc cagaccagaa ggacaaggcc tccttaaaag aggcctgcag	1920
ccccagcaac atcccagcca tccctgcagt catcattaca gatatgggtg ctgaggagga	1980
tggagggcta gaggagatcc aaggaagccc tcgggggtccc ctgcctctga ggaagctgtc	2040
ctcctcctca gcctcctcca ctggcttctc ctcttcttac gatgactcgg aggaggacat	2100
ctccagtga cctgagcgca cgctggaccc caactcagcc tttttgcata ccctggacca	2160
gcagaagccc agagtgaagca agtcatggag aaagataaag aacatgggtg agtgggtccc	2220
ctttgtcatg tccttcaaga agaagtaccc ctggatccag ctggcaggac atgcaggag	2280
cttcaaggca gctgcaaagt gccgcatcct taagaagcac tgtgagtctg agcagcgctg	2340
cctggaccgg ttaatggcgg atgtgctgag acccttcgtg ccagcctacc atggggacgt	2400
ggatgaaggat ggggaacgct acaaccagat ggacgacctg ctggctgact tcgattcgcc	2460
ctgcgtgatg gactgcaaga tgggtgtcag gacatacctg gaggaagaac tcaccaaggc	2520
ccggaagaag cctagcttgc ggaaggacat gtaccagaag atggctcagg tggaccctga	2580

SEQ.Listing.ST25

ggccccact	gaagaggaga	aagcccagcg	agctgtgacc	aagccacggt	acatgcagtg	2640
gcgggaaacc	atcagttcga	cagccaccct	aggcttcagg	atcgaaggca	tcaagaagga	2700
agatggctct	gtgaaccgtg	acttcaagaa	gacaaaaaca	agggagcagg	tcaccgaggc	2760
tttcagagaa	ttcactaagg	gaaaccagaa	catcttgatc	gcctaccggg	accggctgaa	2820
ggccattcga	gcgaccctgg	aaatctctcc	cttcttcaag	tgccacgagg	tcattggcag	2880
ctctctcctc	ttcatccatg	acaagaagga	gcaagccaag	gtgtggatga	ttgacttttg	2940
gaaaaccacg	ccccttccgg	aaggccagac	cctacaacac	gacgtcccct	ggcaggaggg	3000
gaaccgggag	gatggctacc	tctcagggct	ggacaacctc	atcgacatcc	tgacggaaat	3060
gtcccagggc	agccccactca	cctgaggcca	ccgccaccgt	gcatagccgt	gccactttgc	3120
ccgccacctc	tgctgtcgc	ctctctcctc	ccctaattct	tccttttcct	gtctgagcgc	3180
ctacctagaa	cagagcctcc	catctgcact	acaggacact	ttggagaaaa	aaaagagatt	3240
ttttttttct	agatctttac	ttccccggcc	tcctacatag	gggcttgag	gtggcgtttc	3300
tcattgctctc	taaatagaac	caccttctcg	aagagaatta	cacaaagcta	ggccccacat	3360
cctgttacac	tcagagtcgg	cacgggtcca	gaaggccgtg	tgatccctgg	ttgcctaaag	3420
tcttgagaga	ttaagcctcc	ctctgggaga	cactgcccc	ctcccagaaa	attctggccc	3480
acactggcta	ccagtagggg	ccttgctgcc	ccctagtggc	taatgccatc	agtaagcaca	3540
gtcccatttg	tgctctcac	cacgggccct	gaagccagga	cagggacctg	atttctggga	3600
gttgaaa						3608